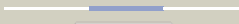
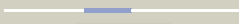


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dcpA_	 Alignment		27.5	14	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein (rafl09-17-b18); PDBTitle: fully automated nmr structure determination of the enth-vhs2 domain at3g16270 from arabidopsis thaliana
2	c1p58F_	 Alignment		25.6	15	PDB header: virus Chain: F: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by 2 9.5 angstrom cryo-em reconstruction
3	c3bs7A_	 Alignment		23.8	12	PDB header: signaling protein Chain: A: PDB Molecule: protein aveugle; PDBTitle: crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
4	c3da4B_	 Alignment		20.5	32	PDB header: antibiotic Chain: B: PDB Molecule: colicin-m; PDBTitle: crystal structure of colicin m, a novel phosphatase2 specifically imported by escherichia coli
5	d1pk1c1	 Alignment		19.0	8	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
6	d1u1ha2	 Alignment		17.0	86	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Cobalamin-independent methionine synthase
7	d2v0ea1	 Alignment		16.8	15	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
8	d2ckca1	 Alignment		16.2	15	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
9	c2ckcA_	 Alignment		16.2	15	PDB header: hydrolase Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 7; PDBTitle: solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
10	c1pk1A_	 Alignment		16.2	8	PDB header: transcription repression Chain: A: PDB Molecule: polyhomeotic-proximal chromatin protein; PDBTitle: hetero sam domain structure of ph and scm.
11	c2rddB_	 Alignment		16.1	23	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.

12	d2ckaa1	Alignment		14.6	21	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
13	c2ckaA_	Alignment		14.6	21	PDB header: hydrolase Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 8; PDBTitle: solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
14	d1tnsa_	Alignment		14.1	63	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
15	c2nq5A_	Alignment		12.8	86	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate-- PDBTitle: crystal structure of methyltransferase from streptococcus2 mutans
16	d1qpma_	Alignment		12.1	13	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
17	d2v0fa1	Alignment		12.1	23	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
18	c3bs5A_	Alignment		11.6	12	PDB header: signaling protein/membrane protein Chain: A: PDB Molecule: protein aveugle; PDBTitle: crystal structure of hcnk2-sam/dhyp-sam complex
19	d2dl6a1	Alignment		11.4	25	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
20	c1u22A_	Alignment		11.0	86	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate-- PDBTitle: a. thaliana cobalamine independent methionine synthase
21	c3d3uA_	Alignment	not modelled	10.4	5	PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26
22	c2ef8A_	Alignment	not modelled	10.2	14	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
23	d1adra_	Alignment	not modelled	10.1	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
24	c3hrqB_	Alignment	not modelled	9.0	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: aflatoxin biosynthesis polyketide synthase; PDBTitle: the product template domain from pksa with palmitate bound
25	d1kw4a_	Alignment	not modelled	8.7	8	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
26	d2axtk1	Alignment	not modelled	8.5	44	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein K, PsbK Family: PsbK-like
27	d1dlca3	Alignment	not modelled	8.5	17	Fold: Toxins' membrane translocation domains Superfamily: delta-Endotoxin (insecticide), N-terminal domain Family: delta-Endotoxin (insecticide), N-terminal domain
28	c2kixD_	Alignment	not modelled	8.4	33	PDB header: transport protein Chain: D: PDB Molecule: bm2 protein; PDBTitle: channel domain of bm2 protein from influenza b virus

29	d1y7ya1	Alignment	not modelled	8.2	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
30	c2jlnA_	Alignment	not modelled	8.0	14	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
31	c3dihA_	Alignment	not modelled	7.9	19	PDB header: toxin Chain: A: PDB Molecule: phospholipase a2 homolog, ammodytin I; PDBTitle: crystal structure of ammodytin I
32	c3l7sA_	Alignment	not modelled	7.8	86	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of mete coordinated with zinc from streptococcus2 mutans
33	c2l35B_	Alignment	not modelled	7.3	33	PDB header: protein binding Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12-nkg2c transmembrane heterotrimer
34	c2l34B_	Alignment	not modelled	7.0	33	PDB header: protein binding Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12 transmembrane homodimer
35	c2l34A_	Alignment	not modelled	7.0	33	PDB header: protein binding Chain: A: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12 transmembrane homodimer
36	d2gmha2	Alignment	not modelled	6.9	14	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: Electron transfer flavoprotein-ubiquinone oxidoreductase-like
37	c3ivpD_	Alignment	not modelled	6.7	14	PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
38	c1a87A_	Alignment	not modelled	6.6	22	PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n
39	d1a87a_	Alignment	not modelled	6.6	22	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
40	d2rlj1l	Alignment	not modelled	6.5	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
41	c3gk7A_	Alignment	not modelled	6.4	11	PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
42	c2oasA_	Alignment	not modelled	6.4	16	PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coenzyme a transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coenzyme a transferase (atoa)2 in complex with coa from shewanella oneidensis, northeast structural3 genomics target sor119.
43	c1nauA_	Alignment	not modelled	6.3	29	PDB header: hormone/growth factor Chain: A: PDB Molecule: glucagon; PDBTitle: nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles
44	c2kdrX_	Alignment	not modelled	6.3	43	PDB header: viral protein, membrane protein Chain: X: PDB Molecule: non-structural protein 4b; PDBTitle: solution structure of hcv ns4b(227-254)
45	c3hefB_	Alignment	not modelled	5.8	13	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit
46	d1lna_	Alignment	not modelled	5.4	15	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: ENTH domain
47	d1pa0a_	Alignment	not modelled	5.3	14	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
48	c1v85A_	Alignment	not modelled	5.3	15	PDB header: apoptosis Chain: A: PDB Molecule: similar to ring finger protein 36; PDBTitle: sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator
49	d1gmza_	Alignment	not modelled	5.2	19	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
50	d1r89a3	Alignment	not modelled	5.2	10	Fold: Ferredoxin-like Superfamily: PAP/Archaeal CCA-adding enzyme, C-terminal domain Family: Archaeal tRNA CCA-adding enzyme
51	c3k8pC_	Alignment	not modelled	5.1	36	PDB header: transport protein/transport protein Chain: C: PDB Molecule: dsl1; PDBTitle: structural basis for vesicle tethering by the dsl1 complex
52	c3bq7A_	Alignment	not modelled	5.1	24	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase delta; PDBTitle: sam domain of diacylglycerol kinase delta1 (e35g)
53	d1hx8a2	Alignment	not modelled	5.1	15	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: Phosphoinositide-binding clathrin adaptor, N-terminal domain
						Fold: Photosystem I subunits PsA/PsB

54	d1jb0a_	Alignment	not modelled	5.1	53	Superfamily: Photosystem I subunits PsaA/PsaB Family: Photosystem I subunits PsaA/PsaB
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